

# SEQUENCE LISTING

<110> NsGene  
Biogen, Inc.  
Johansen, Teit E.  
Sah, Dinah Wen-Yee

<120> Novel Neurotrophic Factors

<130> 00689-511 PCT (C045 CIP) NBN

<140> Filed Herewith

<141> 2002-02-28

<150> DANISH 1998 00904

<151> 1998-07-06

<150> USSN 60/092,229

<151> 1998-07-09

<150> DANISH 1998 01048

<151> 1998-08-19

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<151> 1998-10-13

<150> DANISH 1998 01265

<151> 1998-10-06

<150> U.S.S.N 09/347,613

<151> 1999-07-02

<150> U.S.S.N 09/804,615

<151> 2001-03-12

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<170> PatentIn Ver. 2.1

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<223> DISULFID: Cys72-Cys72 interchain disulfide bridge

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tccccaagcc cacctgggtg ccctctttct ccctgaggct ccacttggtc tctccgcgc 119

atg cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg ctg agc agc 167
Met Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu Leu Ser Ser
-95 -90 -85 -80

gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct gcc ccc cgc 215
Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro Ala Pro Arg
-75 -70 -65

gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac ctg ccg ggg 263
Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
-60 -55 -50

gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg ccg cgc cgc 311
Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
-45 -40 -35

aga cac ttc tcg gcc cgc gcc ccc gcc gcc tgc acc ccc atc tgc tct 359
Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
-30 -25 -20

tcc ccg cgg gtc cgc gcg gcg cgg ctg ggg ggc cgg gca gcg cgc tcg 407
Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
-15 -10 -5 -1 1

ggc agc ggg ggc gcg ggg tgc cgc ctg cgc tcg cag ctg gtg ccg gtg 455
Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
5 10 15

cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg gtg cgt ttc cgc 503
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

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ttc tgc acc ggc tcc tgc ccg cgc gcg cgc tct cca cac gac ctc agc 551
Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
35 40 45

ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg ccc ccg ggc tcc 599
Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
50 55 60 65

cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc tac gaa gcg gtc 647
Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
70 75 80

tcc ttc atg gac gtc aac agc acc tgg aga acc gtg gac cgc ctc tcc 695
Ser Phe Met Ala Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser
85 90 95

gcc acc gcc tgc ggc tgc ctg ggc tgaggggctcg ctccaggggt ttgcagactg 749
Ala Thr Ala Cys Gly Cys Leu Gly
100 105

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gacccttacc ggtggctctt cctgcctggg accctccgc agagtccac tagccagcgg 809

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cctcagccag ggacgaaggc ctcaaagctg agaggcccct gccggtgggt gatgga 865

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-75 -70 -65

Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His Leu Pro Gly
-60 -55 -50

Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg Pro Arg Arg
-45 -40 -35

Arg His Phe Ser Ala Arg Ala Pro Ala Ala Cys Thr Pro Ile Cys Ser
-30 -25 -20

Ser Pro Arg Val Arg Ala Ala Arg Leu Gly Gly Arg Ala Ala Arg Ser
-15 -10 -5 -1 1

Gly Ser Gly Gly Ala Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val
5 10 15

Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg
20 25 30

Phe Cys Thr Gly Ser Cys Pro Arg Ala Arg Ser Pro His Asp Leu Ser
35 40 45

Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser
50 55 60 65

Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val
70 75 80

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Ser	Phe	Met	Asp	Val	Asn	Ser	Thr	Trp	Arg	Thr	Val	Asp	Arg	Leu	Ser
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		100					105								

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 <223> DISULFID: Cys70-Cys136 disulfide bridge

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 <222> (517)..(711)  
 <223> DISULFID: Cys74-Cys138 disulfide bridge

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<222> (616)..(618)

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bridge

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-95 -90 -85	
gtc ctt cct ccc caa gcc cac ctg ggt gcc ctc ttt ctc cct gag gct	96
Val Leu Pro Pro Gln Ala His Leu Gly Ala Leu Phe Leu Pro Glu Ala	
-80 -75 -70	
cca ctt ggt ctc tcc gcg cag cct gcc ctg tgg ccc acc ctg gcc gct	144
Pro Leu Gly Leu Ser Ala Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala	
-65 -60 -55	
ctg gct ctg ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc	192
Leu Ala Leu Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro	
-50 -45 -40	
cgc agc cct gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc	240
Arg Ser Pro Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro	
-35 -30 -25 -20	
gcc ggc cac ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga	288
Ala Gly His Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg	
-15 -10 -5	
gcc cgg cgg ccg ccg ccg cag cct tct ccg ccc gcg ccc ccg ccg cct	336
Ala Arg Arg Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro	
-1 1 5 10	
gca ccc cca tct gct ctt ccc cgc ggg ggc cgc gcg gcg ccg gct ggg	384
Ala Pro Pro Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly	
15 20 25	
ggc ccg ggc aac cgc gct ccg gca gcg ggg gcg ccg ggc tgc cgc ctg	432
Gly Pro Gly Asn Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu	
30 35 40 45	
cgc tcg cag ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc	480
Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser	
50 55 60	
gac gag ctg gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg	528
Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala	
65 70 75	
cgc tct cca cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc	576
Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala	
80 85 90	
ctg cga ccg ccc ccg ggc tcc ccg ccc gtc agc cag ccc tgc tgc cga	624
Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg	
95 100 105	
ccc acg cgc tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg	672
Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp	
110 115 120 125	
aga acc gtg gac cgc ctc tcc gcc aac ccc tgc ggc tgc ctg ggc	717
Arg Thr Val Asp Arg Leu Ser Ala Asn Pro Cys Gly Cys Leu Gly	
130 135 140	



<213> Homo sapiens

<220>

<223> Wherein Xaa at position 134 designates Asn or Thr,  
and Xaa at position 135 designates Ala or Pro

<400> 5

Pro	Pro	Pro	Gln	Pro	Ser	Arg	Pro	Ala	Pro	Pro	Pro	Pro	Ala	Pro	Pro	
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Ser	Ala	Leu	Pro	Arg	Gly	Gly	Arg	Ala	Ala	Arg	Ala	Gly	Gly	Pro	Gly	
			20					25					30			
Asn	Arg	Ala	Arg	Ala	Ala	Gly	Ala	Arg	Gly	Cys	Arg	Leu	Arg	Ser	Gln	
		35					40					45				
Leu	Val	Pro	Val	Arg	Ala	Leu	Gly	Leu	Gly	His	Arg	Ser	Asp	Glu	Leu	
	50					55					60					
Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly	Ser	Cys	Arg	Arg	Ala	Arg	Ser	Pro	
65					70				75						80	
His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly	Ala	Leu	Arg	Pro	
			85						90					95		
Pro	Pro	Gly	Ser	Arg	Pro	Val	Ser	Gln	Pro	Cys	Cys	Arg	Pro	Thr	Arg	
			100					105					110			
Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp	Val	Asn	Ser	Thr	Trp	Arg	Thr	Val	
	115						120					125				
Asp	Arg	Leu	Ser	Ala	Xaa	Xaa	Cys	Gly	Cys	Leu	Gly					
	130					135					140					

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<211> 116

<212> PRT

<213> Homo sapiens

<220>

<223> Wherein Xaa at position 110 designates Asn or Thr,  
and Xaa at position 111 designates Ala or Pro

<400> 6

Ala	Ala	Arg	Ala	Gly	Gly	Pro	Gly	Asn	Arg	Ala	Arg	Ala	Ala	Gly	Ala	
1				5					10					15		
Arg	Gly	Cys	Arg	Leu	Arg	Ser	Gln	Leu	Val	Pro	Val	Arg	Ala	Leu	Gly	
			20					25					30			
Leu	Gly	His	Arg	Ser	Asp	Glu	Leu	Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly	
		35					40					45				
Ser	Cys	Arg	Arg	Ala	Arg	Ser	Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	
	50					55				60						
Leu	Gly	Ala	Gly	Ala	Leu	Arg	Pro	Pro	Pro	Gly	Ser	Arg	Pro	Val	Ser	
65					70					75					80	
Gln	Pro	Cys	Cys	Arg	Pro	Thr	Arg	Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp	
				85					90					95		
Val	Asn	Ser	Thr	Trp	Arg	Thr	Val	Asp	Arg	Leu	Ser	Ala	Xaa	Xaa	Cys	





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<221> mat\_peptide

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<222> (379)..(717)

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<223> CARBOHYD: glycosylated asparagine at Asn122

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<222> (424)..(621)

<223> DISULFID: Gly43-Gly108 disulfide bridge

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<223> DISULFID: Gly74-Gly138 disulfide bridge

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<222> (616)..(618)

<223> DISULFID: Gly107-Gly107 interchain disulfide bridge

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aggagggtgg gggaacagct caacaatggc tgatgggcgc tcctggtggt gatagag 57

atg gaa ctt gga ctt gga ggc ctc tcc acg ctg tcc cac tgc ccc tgg 105  
Met Glu Leu Gly Leu Gly Gly Leu Ser Thr Leu Ser His Cys Pro Trp  
-80 -75 -70 -65

cct agg cgg cag cct gcc ctg tgg ccc acc ctg gcc gct ctg gct ctg 153  
Pro Arg Arg Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu  
-60 -55 -50

ctg agc agc gtc gca gag gcc tcc ctg ggc tcc gcg ccc cgc agc cct 201  
Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro  
-45 -40 -35

gcc ccc cgc gaa ggc ccc ccg cct gtc ctg gcg tcc ccc gcc ggc cac 249  
Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His  
-30 -25 -20

ctg ccg ggg gga cgc acg gcc cgc tgg tgc agt gga aga gcc cgg cgg 297  
Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg  
-15 -10 -5 -1

ccg ccg ccg cag cct tct cgg ccc gcg ccc ccg ccg cct gca ccc cca 345  
Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
1 5 10 15

tct gct ctt ccc cgc ggg ggc cgc gcg gcg cgg gct ggg ggc ccg ggc 393

Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
                     20                    25                    30  
 agc cgc gct cgg gca gcg ggg gcg cgg ggc tgc cgc ctg cgc tcg cag 441  
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
                     35                    40                    45  
 ctg gtg ccg gtg cgc gcg ctc ggc ctg ggc cac cgc tcc gac gag ctg 489  
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
                     50                    55                    60  
 gtg cgt ttc cgc ttc tgc agc ggc tcc tgc cgc cgc gcg cgc tct cca 537  
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
                     65                    70                    75                    80  
 cac gac ctc agc ctg gcc agc cta ctg ggc gcc ggg gcc ctg cga ccg 585  
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
                     85                    90                    95  
 ccc ccg ggc tcc cgg ccc gtc agc cag ccc tgc tgc cga ccc acg cgc 633  
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
                     100                    105                    110  
 tac gaa gcg gtc tcc ttc atg gac gtc aac agc acc tgg aga acc gtg 681  
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
                     115                    120                    125  
 gac cgc ctc tcc gcc acc gcc tgc ggc tgc ctg ggc tgagggctcg 727  
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
                     130                    135                    140  
 ctccaggggt ttgcagactg gacccttacc ggtggctctt cctgcctggg accctcccgc 787  
 agagtcccac tagccagcgg cctcagccag ggacgaaggc ctcaaagctg agaggcccct 847  
 accggtgggt gatg 861

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                     -60                    -55                    -50  
 Leu Ser Ser Val Ala Glu Ala Ser Leu Gly Ser Ala Pro Arg Ser Pro  
                     -45                    -40                    -35  
 Ala Pro Arg Glu Gly Pro Pro Pro Val Leu Ala Ser Pro Ala Gly His  
                     -30                    -25                    -20  
 Leu Pro Gly Gly Arg Thr Ala Arg Trp Cys Ser Gly Arg Ala Arg Arg  
                     -15                    -10                    -5                    -1  
 Pro Pro Pro Gln Pro Ser Arg Pro Ala Pro Pro Pro Pro Ala Pro Pro  
   1                    5                    10                    15  
 Ser Ala Leu Pro Arg Gly Gly Arg Ala Ala Arg Ala Gly Gly Pro Gly  
                     20                    25                    30

Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
           35                          40                          45  
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
           50                          55                          60  
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
           65                          70                          75                          80  
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
                           85                          90                          95  
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
                           100                          105                          110  
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
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 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
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                           20                          25                          30  
 Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
           35                          40                          45  
 Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
           50                          55                          60  
 Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
           65                          70                          75                          80  
 His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
                           85                          90                          95  
 Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
                           100                          105                          110  
 Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
           115                          120                          125  
 Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
           130                          135                          140

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20 25 30  
Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly  
35 40 45  
Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu  
50 55 60  
Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser  
65 70 75 80  
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
85 90 95  
Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys  
100 105 110  
Gly Cys Leu Gly  
115

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20 25 30  
Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg  
35 40 45  
Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala  
50 55 60  
Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys  
65 70 75 80  
Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser  
85 90 95

Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu  
 100 105 110

Gly

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 cccgggtccc ggccgatcag ccagccctgc tgccggccca ctgcgtatga ggccgtctcc 180  
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 cggatccgga ggggtggagcg gccaggtagg ccctgaaagg tggggcgggg cgggggcgct 180  
 ctggggccca ccccgggatc tgggtgacgcc ggggctggaa tttgacaccg gacggcgggc 240  
 ggcaggaggc tgctgaggga tggagttggg ctcgggcccc agatgcggcc cgcgggctct 300  
 gccagcaaca agtccctcgg gccccagccc tcgctgcgac tggggcttgg agccctgcac 360  
 ccaagggcac agaccggctg ccaaggcccc acttttaact aaaagaggcg ctgccagggtg 420  
 cacaactctg ggcatgatcc acttgagctt cgggggaaag ccagcactg gtcccaggag 480  
 aggcgcctag aaggacacgg accaggaccc ctttggtatg gaggtaacgc tgagcatgga 540  
 gtggaaggaa ctcaagttac tactttctcc aaccaccctg gtaccttcag ccctgaagta 600  
 cagagcagaa gggctcttaga agacaggacc acagctgtgt gaggctcccc cctgaggcct 660  
 tagacgatct ctgagctcag ctgagctttg tttgcccatc tggagaagtg agccattgat 720  
 tgaccttgtg gcacgcgaa ggaacaggtc ctgccaaagc cctaacacag agagcaagg 780

tctccatcgc agctaccgct gctgagttga ctctagctac tccaacctcc tgggtcgctt	840
cgagagactg gagtggaagg aggaataccc caaaggataa ctaactcatc tttcagtttg	900
caagctgccg caggaagagg gtgggggaaac ggggtccacga aggcttctga tgggagcttc	960
tggagccgaa agct atg gaa ctg gga ctt gca gag cct act gca ttg tcc	1010
Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser	
1 5 10	
cac tgc ctc cgg cct agg tgg cag tca gcc tgg tgg cca acc cta gct	1058
His Cys Leu Arg Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala	
15 20 25	
gtt cta gcc ctg ctg agc tgc gtc aca gaa gct tcc ctg gac cca atg	1106
Val Leu Ala Leu Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met	
30 35 40	
tcc cgc agc ccc gcc gct cgc gac ggt ccc tca ccg gtc ttg gcg ccc	1154
Ser Arg Ser Pro Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro	
45 50 55 60	
ccc acg gac cac ctg cct ggg gga cac act gcg cat ttg tgc agc gaa	1202
Pro Thr Asp His Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu	
65 70 75	
aga acc ctg cga ccc ccg cct cag tct cct cag ccc gca ccc ccg ccg	1250
Arg Thr Leu Arg Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro	
80 85 90	
cct ggt ccc gcg ctc cag tct cct ccc gct gcg ctc cgc ggg gca cgc	1298
Pro Gly Pro Ala Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg	
95 100 105	
gcg gcg cgt gca gga acc ccg agc agc cgc gca ccg acc aca gat gcg	1346
Ala Ala Arg Ala Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala	
110 115 120	
cgc ggc tgc cgc ctg cgc tgc cag ctg gtg ccg gtg agc gcg ctc ggc	1394
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly	
125 130 135 140	
cta ggc cac agc tcc gac gag ctg ata cgt ttc cgc ttc tgc agc ggc	1442
Leu Gly His Ser Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly	
145 150 155	
tgc tgc cgc cga gca cgc tcc cag cac gat ctc agt ctg gcc agc cta	1490
Ser Cys Arg Arg Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu	
160 165 170	
ctg ggc gct ggg gcc cta ccg tgc cct ccc ggg tcc ccg ccg atc agc	1538
Leu Gly Ala Gly Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser	
175 180 185	
cag ccc tgc tgc cgg ccc act cgc tat gag gcc gtc tcc ttc atg gac	1586
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp	
190 195 200	
gtg aac agc acc tgg agg acc gtg gac cac ctc tcc gcc act gcc tgc	1634
Val Asn Ser Thr Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys	
205 210 215 220	
ggc tgt ctg ggc tgaggatgat ctatctccaa gcctttgcac actagaccca	1686

Gly Cys Leu Gly

tgtgttgccc tacctggaac agctccaccg ggcctcacta accaggagcc tcaactcagc 1746  
aggatatgga ggctgcagag ctcaggcccc aggccggtga gtgacagacg tcgtcggcat 1806  
gacagacaga gtgaaagatg tcggaaccac tgaccaacag tcccaagttg ttcattggatc 1866  
ccagctctac agacaggaga aacctcagct aaagagaact cctctgggag aatccagaaa 1926  
tggccctctg tcttggggaa tgaattttga agagatatat atacatatat acattgtagt 1986  
cgcgttgctg gaccagcctg tgctgaaacc agtcccgtgt tcacttgtgg aagccgaagc 2046  
cctattttatt atttctaaat tattttattta ctttgaaaaa aaacggccaa gtcggcctcc 2106  
ctttagttag gggttaatttg tgatcccggg 2136

<210> 16  
<211> 224  
<212> PRT  
<213> Murinae gen. sp.

<400> 16  
Met Glu Leu Gly Leu Ala Glu Pro Thr Ala Leu Ser His Cys Leu Arg  
1 5 10 15  
Pro Arg Trp Gln Ser Ala Trp Trp Pro Thr Leu Ala Val Leu Ala Leu  
20 25 30  
Leu Ser Cys Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro  
35 40 45  
Ala Ala Arg Asp Gly Pro Ser Pro Val Leu Ala Pro Pro Thr Asp His  
50 55 60  
Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Thr Leu Arg  
65 70 75 80  
Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Gly Pro Ala  
85 90 95  
Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala  
100 105 110  
Gly Thr Arg Ser Ser Arg Ala Arg Thr Thr Asp Ala Arg Gly Cys Arg  
115 120 125  
Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser  
130 135 140  
Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg  
145 150 155 160  
Ala Arg Ser Gln His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly  
165 170 175  
Ala Leu Arg Ser Pro Pro Gly Ser Arg Pro Ile Ser Gln Pro Cys Cys  
180 185 190  
Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr  
195 200 205

Trp Arg Thr Val Asp His Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
210 215 220

<210> 17  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 17  
cctggccagc ctactggg 18

<210> 18  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 18  
aaggagaccg cttcgtagcg 20

<210> 19  
<211> 17  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 19  
atggaacttg gacttgg 17

<210> 20  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 20  
tccatcaccc accggc 16

<210> 21  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR Primer

<400> 21  
ggccaccgct ccgacgag 18



<210> 22  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 22  
 ggcggtccac ggttctccag 20  
  
 <210> 23  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 23  
 ccaagcccac ctgggtgccc tctttctcc 29  
  
 <210> 24  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 24  
 catcaccac cggcaggggc ctctcag 27  
  
 <210> 25  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 25  
 gagcccatgc ccggcctgat ctcagcccga ggaca 35  
  
 <210> 26  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: PCR Primer  
  
 <400> 26  
 ccctggctga ggccgctggc tagtgggact ctgc 34  
  
 <210> 27  
 <211> 31  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Hybridization Probe

<220>

<221> misc\_structure

<222> (1)

<223> wherein n represents a conjugant moiety linking to alkaline phosphatase

<400> 27

ncaggtggtc cgtggggggc gccaaagaccg g

31

<210> 28

<211> 16

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 28

ctaggagccc atgccc

16

<210> 29

<211> 351

<212> DNA

<213> Homo sapiens

<400> 29

atggctggag gaccgggac tcgtgctcgt gcagcaggag cacgtggctg tcgtctgcgt 60  
tctcaactag tgccggtgcg tgcactcgga ctgggacacc gttccgacga actagtacgt 120  
tttcgttttt gtccaggatc ttgtcgtcgt gcacgttctc cgcacgatct atctctagca 180  
tctctactag gagccggagc actaagaccg ccgccgggat ctagacctgt atctcaacct 240  
tggtgtagac ctactagata cgaagcagta tctttcatgg acgtaaactc tacatggaga 300  
accgtagata gactatctgc aaccgcatgt ggctgtctag gatgataata g 351

<210> 30

<211> 414

<212> DNA

<213> Homo sapiens

<400> 30

atgggccatc atcatcatca tcatcatcat catcactcga gcggccatat cgacgacgac 60  
gacaaggctg gaggaccggg atctcgtgct cgtgcagcag gagcacgtgg ctgtcgtctg 120  
cgttctcaac tagtgccggt gcgtgcactc ggactgggac accgttccga cgaactagta 180  
cgttttcgtt ttgtttcagg atcttgctcgt cgtgcacgtt ctccgcatga tctatctcta 240  
gcatctctac taggagccgg agcactaaga ccgccgccgg gatctagacc tgtatctcaa 300  
ccttgttgta gacctactag atacgaagca gtatctttca tggacgtaaa ctctacatgg 360  
agaaccgtag atagactatc tgcaaccgca tgtggctgtc taggatgata atag 414

<210> 31

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 31  
aaggaaaaaa gcggccgcca tggaacttgg acttggagg 39

<210> 32  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 32  
ttttttcctt ggcggccgct cagcccaggc agccgcagg 39

<210> 33  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 33  
gagcgagccc tcagcc 16

<210> 34  
<211> 224  
<212> PRT  
<213> Rattus sp.

<400> 34  
Met Glu Leu Gly Leu Gly Glu Pro Thr Ala Leu Ser His Cys Leu Arg  
1 5 10 15  
Pro Arg Trp Gln Pro Ala Leu Trp Pro Thr Leu Ala Ala Leu Ala Leu  
20 25 30  
Leu Ser Ser Val Thr Glu Ala Ser Leu Asp Pro Met Ser Arg Ser Pro  
35 40 45  
Ala Ser Arg Asp Val Pro Ser Pro Val Leu Ala Pro Pro Thr Asp Tyr  
50 55 60  
Leu Pro Gly Gly His Thr Ala His Leu Cys Ser Glu Arg Ala Leu Arg  
65 70 75 80  
Pro Pro Pro Gln Ser Pro Gln Pro Ala Pro Pro Pro Pro Gly Pro Ala  
85 90 95  
Leu Gln Ser Pro Pro Ala Ala Leu Arg Gly Ala Arg Ala Ala Arg Ala  
100 105 110  
Gly Thr Arg Ser Ser Arg Ala Arg Ala Thr Asp Ala Arg Gly Cys Arg  
115 120 125  
Leu Arg Ser Gln Leu Val Pro Val Ser Ala Leu Gly Leu Gly His Ser  
130 135 140  
Ser Asp Glu Leu Ile Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg  
145 150 155 160

Ala	Arg	Ser	Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly
				165					170					175	
Ala	Leu	Arg	Ser	Pro	Pro	Gly	Ser	Arg	Pro	Ile	Ser	Gln	Pro	Cys	Cys
			180					185					190		
Arg	Pro	Thr	Arg	Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp	Val	Asn	Ser	Thr
		195					200					205			
Trp	Arg	Thr	Val	Asp	His	Leu	Ser	Ala	Thr	Ala	Cys	Gly	Cys	Leu	Gly
	210					215					220				

<210> 35  
 <211> 112  
 <212> PRT  
 <213> Homo sapiens

<400> 35															
Gly	Gly	Pro	Gly	Ser	Arg	Ala	Arg	Ala	Ala	Gly	Ala	Arg	Gly	Cys	Arg
1				5					10					15	
Leu	Arg	Ser	Gln	Leu	Val	Pro	Val	Arg	Ala	Leu	Gly	Leu	Gly	His	Arg
			20					25					30		
Ser	Asp	Glu	Leu	Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly	Ser	Cys	Arg	Arg
		35					40					45			
Ala	Arg	Ser	Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly
		50				55					60				
Ala	Leu	Arg	Pro	Pro	Pro	Gly	Ser	Arg	Pro	Val	Ser	Gln	Pro	Cys	Cys
	65				70					75				80	
Arg	Pro	Thr	Arg	Tyr	Glu	Ala	Val	Ser	Phe	Met	Asp	Val	Asn	Ser	Thr
				85					90					95	
Trp	Arg	Thr	Val	Asp	Arg	Leu	Ser	Ala	Thr	Ala	Cys	Gly	Cys	Leu	Gly
			100					105					110		

<210> 36  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 36															
Gly	Pro	Gly	Ser	Arg	Ala	Arg	Ala	Ala	Gly	Ala	Arg	Gly	Cys	Arg	Leu
1				5					10					15	
Arg	Ser	Gln	Leu	Val	Pro	Val	Arg	Ala	Leu	Gly	Leu	Gly	His	Arg	Ser
			20					25					30		
Asp	Glu	Leu	Val	Arg	Phe	Arg	Phe	Cys	Ser	Gly	Ser	Cys	Arg	Arg	Ala
		35					40					45			
Arg	Ser	Pro	His	Asp	Leu	Ser	Leu	Ala	Ser	Leu	Leu	Gly	Ala	Gly	Ala

50                      55                      60  
 Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg  
 65                      70                      75                      80  
 Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp  
 85                      90                      95  
 Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
 100                      105                      110

<210> 37  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 37  
 Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg  
 1                      5                      10                      15  
 Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp  
 20                      25                      30  
 Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg  
 35                      40                      45  
 Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu  
 50                      55                      60  
 Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro  
 65                      70                      75                      80  
 Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg  
 85                      90                      95  
 Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
 100                      105                      110

<210> 38  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 38  
 Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser  
 1                      5                      10                      15  
 Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu  
 20                      25                      30  
 Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser  
 35                      40                      45  
 Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg  
 50                      55                      60  
 Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr  
 65                      70                      75                      80  
 Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr  
 85                      90                      95

Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
100 105

<210> 39  
<211> 108  
<212> PRT  
<213> Homo sapiens

<400> 39  
Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln  
1 5 10 15  
Leu Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu  
20 25 30  
Val Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro  
35 40 45  
His Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro  
50 55 60  
Pro Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg  
65 70 75 80  
Tyr Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val  
85 90 95  
Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
100 105

<210> 40  
<211> 107  
<212> PRT  
<213> Homo sapiens

<400> 40  
Arg Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu  
1 5 10 15  
Val Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val  
20 25 30  
Arg Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His  
35 40 45  
Asp Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro  
50 55 60  
Pro Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr  
65 70 75 80  
Glu Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp  
85 90 95  
Arg Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
100 105

<210> 41  
<211> 106  
<212> PRT  
<213> Homo sapiens

<400> 41

Ala Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val  
1 5 10 15  
Pro Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg  
20 25 30  
Phe Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp  
35 40 45  
Leu Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro  
50 55 60  
Gly Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu  
65 70 75 80  
Ala Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg  
85 90 95  
Leu Ser Ala Thr Ala Cys Gly Cys Leu Gly  
100 105

<210> 42

<211> 105

<212> PRT

<213> Homo sapiens

<400> 42

Arg Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro  
1 5 10 15  
Val Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe  
20 25 30  
Arg Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu  
35 40 45  
Ser Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly  
50 55 60  
Ser Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala  
65 70 75 80  
Val Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu  
85 90 95  
Ser Ala Thr Ala Cys Gly Cys Leu Gly  
100 105

<210> 43

<211> 104

<212> PRT

<213> Homo sapiens

<400> 43

Ala Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val  
1 5 10 15  
Arg Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg  
20 25 30

Phe Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser  
                   35                                  40                                  45  
 Leu Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser  
           50                                  55                                  60  
 Arg Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val  
   65                                  70                                  75                                  80  
 Ser Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser  
                   85                                  90                                  95  
 Ala Thr Ala Cys Gly Cys Leu Gly  
                   100

<210> 44  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg  
   1                                  5                                  10                                  15  
 Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe  
                   20                                  25                                  30  
 Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu  
                   35                                  40                                  45  
 Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg  
           50                                  55                                  60  
 Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser  
   65                                  70                                  75                                  80  
 Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala  
                   85                                  90                                  95  
 Thr Ala Cys Gly Cys Leu Gly  
                   100

<210> 45  
 <211> 102  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala  
   1                                  5                                  10                                  15  
 Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys  
                   20                                  25                                  30  
 Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala  
                   35                                  40                                  45  
 Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro  
           50                                  55                                  60  
 Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe  
   65                                  70                                  75                                  80



Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr  
85 90 95

Ala Cys Gly Cys Leu Gly  
100

<210> 46  
<211> 101  
<212> PRT  
<213> Homo sapiens

<400> 46  
Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu  
1 5 10 15  
Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser  
20 25 30  
Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser  
35 40 45  
Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val  
50 55 60  
Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met  
65 70 75 80  
Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala  
85 90 95  
Cys Gly Cys Leu Gly  
100

<210> 47  
<211> 100  
<212> PRT  
<213> Homo sapiens

<400> 47  
Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly  
1 5 10 15  
Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly  
20 25 30  
Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu  
35 40 45  
Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser  
50 55 60  
Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp  
65 70 75 80  
Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys  
85 90 95  
Gly Cys Leu Gly  
100

<210> 48  
<211> 99  
<212> PRT  
<213> Homo sapiens

<400> 48  
Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu  
1 5 10 15  
Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser  
20 25 30  
Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu  
35 40 45  
Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln  
50 55 60  
Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val  
65 70 75 80  
Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly  
85 90 95  
Cys Leu Gly

<210> 49  
<211> 197  
<212> PRT  
<213> Homo sapiens

<400> 49  
Met Gln Arg Trp Lys Ala Ala Ala Leu Ala Ser Val Leu Cys Ser Ser  
1 5 10 15  
Val Leu Ser Ile Trp Met Cys Arg Glu Gly Leu Leu Leu Ser His Arg  
20 25 30  
Leu Gly Pro Ala Leu Val Pro Leu His Arg Leu Pro Arg Thr Leu Asp  
35 40 45  
Ala Arg Ile Ala Arg Leu Ala Gln Tyr Arg Ala Leu Leu Gln Gly Ala  
50 55 60  
Pro Asp Ala Met Glu Leu Arg Glu Leu Thr Pro Trp Ala Gly Arg Pro  
65 70 75 80  
Pro Gly Pro Arg Arg Arg Ala Gly Pro Arg Arg Arg Arg Ala Arg Ala  
85 90 95  
Arg Leu Gly Ala Arg Pro Cys Gly Leu Arg Glu Leu Glu Val Arg Val  
100 105 110  
Ser Glu Leu Gly Leu Gly Tyr Ala Ser Asp Glu Thr Val Leu Phe Arg  
115 120 125  
Tyr Cys Ala Gly Ala Cys Glu Ala Ala Ala Arg Val Tyr Asp Leu Gly  
130 135 140  
Leu Arg Arg Leu Arg Gln Arg Arg Arg Leu Arg Arg Glu Arg Val Arg  
145 150 155 160

Ala Gln Pro Cys Cys Arg Pro Thr Ala Tyr Glu Asp Glu Val Ser Phe  
165 170 175  
Leu Asp Ala His Ser Arg Tyr His Thr Val His Glu Leu Ser Ala Arg  
180 185 190  
Glu Cys Ala Cys Val  
195

<210> 50  
<211> 156  
<212> PRT  
<213> Homo sapiens

<400> 50  
Met Ala Val Gly Lys Phe Leu Leu Gly Ser Leu Leu Leu Leu Ser Leu  
1 5 10 15  
Gln Leu Gly Gln Gly Trp Gly Pro Asp Ala Arg Gly Val Pro Val Ala  
20 25 30  
Asp Gly Glu Phe Ser Ser Glu Gln Val Ala Lys Ala Gly Gly Thr Trp  
35 40 45  
Leu Gly Thr His Arg Pro Leu Ala Arg Leu Arg Arg Ala Leu Ser Gly  
50 55 60  
Pro Cys Gln Leu Trp Ser Leu Thr Leu Ser Val Ala Glu Leu Gly Leu  
65 70 75 80  
Gly Tyr Ala Ser Glu Lys Val Ile Phe Arg Tyr Cys Ala Gly Ser  
85 90 95  
Cys Pro Arg Gly Ala Arg Thr Gln His Gly Leu Ala Leu Ala Arg Leu  
100 105 110  
Gln Gly Gln Gly Arg Ala His Gly Gly Pro Cys Cys Arg Pro Thr Arg  
115 120 125  
Tyr Thr Asp Val Ala Phe Leu Asp Asp Arg His Arg Trp Gln Arg Leu  
130 135 140  
Pro Gln Leu Ser Ala Ala Ala Cys Gly Cys Gly Gly  
145 150 155

<210> 51  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 51  
Met Lys Leu Trp Asp Val Val Ala Val Cys Leu Val Leu Leu His Thr  
1 5 10 15  
Ala Ser Ala Phe Pro Leu Pro Ala Gly Lys Arg Pro Pro Glu Ala Pro  
20 25 30  
Ala Glu Asp Arg Ser Leu Gly Arg Arg Arg Ala Pro Phe Ala Leu Ser  
35 40 45  
Ser Asp Ser Asn Met Pro Glu Asp Tyr Pro Asp Gln Phe Asp Asp Val  
50 55 60

Met Asp Phe Ile Gln Ala Thr Ile Lys Arg Leu Lys Arg Ser Pro Asp  
65 70 75 80

Lys Gln Met Ala Val Leu Pro Arg Arg Glu Arg Asn Arg Gln Ala Ala  
85 90 95

Ala Ala Asn Pro Glu Asn Ser Arg Gly Lys Gly Arg Arg Gly Gln Arg  
100 105 110

Gly Lys Asn Arg Gly Cys Val Leu Thr Ala Ile His Leu Asn Val Thr  
115 120 125

Asp Leu Gly Leu Gly Tyr Glu Thr Lys Glu Glu Leu Ile Phe Arg Tyr  
130 135 140

Cys Ser Gly Ser Cys Asp Ala Ala Glu Thr Thr Tyr Asp Lys Ile Leu  
145 150 155 160

Lys Asn Leu Ser Arg Asn Arg Arg Leu Val Ser Asp Lys Val Gly Gln  
165 170 175

Ala Cys Cys Arg Pro Ile Ala Phe Asp Asp Asp Leu Ser Phe Leu Asp  
180 185 190

Asp Asn Leu Val Tyr His Ile Leu Arg Lys His Ser Ala Lys Arg Cys  
195 200 205

Gly Cys Ile  
210

<210> 52  
<211> 365  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic gene  
for Neublastin

<400> 52  
taccatggct ggaggaccgg gatctcgtgc tcgtgcagca ggagcacgtg gctgtcgtct 60  
gcgttctcaa ctagtgccgg tgcgtgcact cggactggga caccgttccg acgaactagt 120  
acgttttcgt ttttgttcag gatcttgctg tcgtgcacgt tctccgcatg atctatctct 180  
agcatctcta ctaggagccg gagcactaag accgccgccg ggatctagac ctgtatctca 240  
accttggtgt agacctacta gatacgaagc agtatctttc atggacgtaa actctacatg 300  
gagaaccgta gatagactat ctgcaaccgc atgtggctgt ctaggatgat aatagggatc 360  
cggct 365

<210> 53  
<211> 365  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:synthetic gene  
for Neublastin

<400> 53  
atggtaccga cctcctggcc cttagagcag agcacgtcgt cctcgtgcac cgacagcaga 60  
cgcaagagtt gatcacggcc accgacgtga gcctgacct gtggcaaggc tgcttgatca 120  
tgcaaaagca aaaacaagtc ctagaacagc agcacgtgca agaggcgtac tagatagaga 180

```

tcgtagagat gatcctcggc ctcgtgattc tggcggcggc cctagatctg gacatagagt 240
tggaacaaca tctggatgat ctatgcttcg tcatagaaag tacctgcatt tgagatgtac 300
ctcttggcat ctatctgata gacgttggcg tacaccgaca gatcctacta ttatccctag 360
gccga 365

```

```

<210> 54
<211> 114
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:synthetic
      Neublabin

```

```

<400> 54
Met Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala Ala Gly Ala Arg Gly
  1             5             10             15
Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg Ala Leu Gly Leu Gly
             20             25             30
His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe Cys Ser Gly Ser Cys
             35             40             45
Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu Ala Ser Leu Leu Gly
             50             55             60
Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg Pro Val Ser Gln Pro
             65             70             75             80
Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser Phe Met Asp Val Asn
             85             90             95
Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala Thr Ala Cys Gly Cys
             100            105            110
Leu Gly

```

```

<210> 55
<211> 442
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:synthetic gene
      for HisNeublabin

```

```

<400> 55
taccatgggc catcatcatc atcatcatca tcatcatcac tcgagcggcc atatcgacga 60
cgacgacaag gctggaggac cgggatctcg tgctcgtgca gcaggagcac gtggctgtcg 120
tctgcgttct caactagtgc cgggtgcgtgc actcggactg ggacaccggt ccgacgaact 180
agtacgtttt cgtttttgtt caggatcttg tcgtcgtgca cgttctccgc atgatctatc 240
tctagcatct ctactaggag ccggagcact aagaccgccg ccgggatcta gacctgtatc 300
tcaaccttgt tgtagaccta ctagatacga agcagtatct ttcatggacg taaactctac 360
atggagaacc gtagatagac tatctgcaac cgcattgtggc tgtctaggat gataataggg 420
atccggctgc taacaaagcc cg 442

```

```

<210> 56
<211> 442
<212> DNA

```

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic gene  
for HisNeublastin

<400> 56

```
atggtacccg gtagtagtag tagtagtagt agtagtagtg agctcgccgg tatagctgct 60
gctgctgttc cgacctcctg gccctagagc acgagcacgt cgtcctcgtg caccgacagc 120
agacgcaaga gttgatcacg gccacgcacg tgagcctgac cctgtggcaa ggctgcttga 180
tcatgcaaaa gcaaaaacaa gtcctagaac agcagcacgt gcaagaggcg tactagatag 240
agatcgtaga gatgatcctc ggctcgtga ttctggcggc ggccctagat ctggacatag 300
agttggaaca acatctggat gatctatgct tcgtcataga aagtacctgc atttgagatg 360
tacctcttgg catctatctg atagacgttg gcgtacaccg acagatccta ctattatccc 420
taggcgcagc attgtttcgg gc
```

<210> 57

<211> 135

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:synthetic  
HisNeublastin

<400> 57

```
Met Gly His His His His His His His His His Ser Ser Gly His
 1          5          10          15

Ile Asp Asp Asp Asp Lys Ala Gly Gly Pro Gly Ser Arg Ala Arg Ala
 20          25          30

Ala Gly Ala Arg Gly Cys Arg Leu Arg Ser Gln Leu Val Pro Val Arg
 35          40          45

Ala Leu Gly Leu Gly His Arg Ser Asp Glu Leu Val Arg Phe Arg Phe
 50          55          60

Cys Ser Gly Ser Cys Arg Arg Ala Arg Ser Pro His Asp Leu Ser Leu
 65          70          75          80

Ala Ser Leu Leu Gly Ala Gly Ala Leu Arg Pro Pro Pro Gly Ser Arg
 85          90          95

Pro Val Ser Gln Pro Cys Cys Arg Pro Thr Arg Tyr Glu Ala Val Ser
100          105          110

Phe Met Asp Val Asn Ser Thr Trp Arg Thr Val Asp Arg Leu Ser Ala
115          120          125

Thr Ala Cys Gly Cys Leu Gly
130          135
```